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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/824,134

DATE: 06/26/2001

TIME: 15:11:31

Input Set : N:\Crf3\RULE60\09824134.txt

Output Set: N:\CRF3\06262001\I824134.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: WALLACH, David
7 BOLDIN, Mark
8 VARFOLOMEEV, Eugene
9 METT, Igor

11 (ii) TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
12 RECEPTORS

14 (iii) NUMBER OF SEQUENCES: 2

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
18 (B) STREET: 419 Seventh Street N.W., Ste. 300
19 (C) CITY: Washington
20 (D) STATE: D.C.
21 (E) COUNTRY: United States of America
22 (F) ZIP: 20004

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/824,134
C--> 32 (B) FILING DATE: 03-Apr-2001

46 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/860,082
36 (B) FILING DATE:
39 (A) APPLICATION NUMBER: IL 112022
40 (B) FILING DATE: 15-DEC-1994
43 (A) APPLICATION NUMBER: IL 112692
44 (B) FILING DATE: 19-FEB-1995
47 (A) APPLICATION NUMBER: IL 114615
48 (B) FILING DATE: 16-JUL-1995

50 (viii) ATTORNEY/AGENT INFORMATION:

51 (A) NAME: BROWDY, Roger L.
52 (B) REGISTRATION NUMBER: 25,618
53 (C) REFERENCE/DOCKET NUMBER: WALLACH=16

55 (ix) TELECOMMUNICATION INFORMATION:

56 (A) TELEPHONE: (202) 628-5197
57 (B) TELEFAX: (202) 737-3528

60 (2) INFORMATION FOR SEQ ID NO: 1:

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 1701 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: single
66 (D) TOPOLOGY: linear

68 (ii) MOLECULE TYPE: cDNA

ENTERED

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70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 1..768
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 GTG AAT CAG GCA CCG GAG TGC AGG TTC GGG GGT GGA ATC CTT GGG CCG      48
77 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
78   1      5      10      15
80 CTG GGC AAG CGG CGA GAC CTG GCC AGG GCC AGC GAG CCG AGG ACA GAG      96
81 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
82      20      25      30
84 GGC GCG CGG AGG GCC GGG CCG CAG CCC CGG CCG CTT GCA GAC CCC GCC      144
85 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
86      35      40      45
88 ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC AGC CTG TCG      192
89 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
90      50      55      60
92 AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG CGC GTG GTC      240
93 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
94 65      70      75      80
96 AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC TTC TCC ATG      288
97 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
98      85      90      95
100 CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG CTC CTG CGC      336
101 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
102      100      105      110
104 GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG CGC GTC GAC      384
105 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
106      115      120      125
108 GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG GAA GAA GAC      432
109 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
110      130      135      140
112 CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG AAA GAT TGG      480
113 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
114 145      150      155      160
116 AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG ATC GAC AGC      528
117 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
118      165      170      175
120 ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG CGG GAG TCA      576
121 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
122      180      185      190
124 CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA GTG GCC CAC      624
125 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
126      195      200      205
128 CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG GCT GAC CTG      672
129 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
130      210      215      220
132 GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG AGT GGG GCC      720
133 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
134 225      230      235      240

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136 ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC GAA GCG TCC      768
137 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
138                               245                               250                               255
140 TGATGGGCCG CTGCTTTGCG CTGGTGGACC ACAGGCATCT ACACAGCCTG GACTTTGGTT      828
142 CTCTCCAGGA AGGTAGCCCA GCACTGTGAA GACCCAGCAG GAAGCCAGGC TGAGTGAGCC      888
144 ACAGACCACC TGCTTCTGAA CTCAAGCTGC GTTTATTAAT GCCTCTCCCG CACCAGGCCG      948
146 GGCTTGGGCC CTGCACAGAT ATTTCCATTT CTCCTCACT ATGACACTGA GCAAGATCTT     1008
148 GTCTCCACTA AATGAGCTCC TGCAGGAGTA GTTGAAAGT TGGAACCGTG TCCAGCACAG     1068
150 AAGGAATCTG TGCAGATGAG CAGTCACACT GTTACTCCAC AGCGGAGGAG ACCAGCTCAG     1128
152 AGGCCCAGGA ATCGGAGCGA AGCAGAGAGG TGGAGAAGT GGATTTGAAC CCCC GCCATC     1188
154 CTTACACAGA GCCCATGCTC AACCCTGTG GCGTTCTGCT GCCCTGCAG TTGGCAGAAA     1248
156 GGATGTTTTT GTCCCATTTT CTTGGAGGCC ACCGGGACAG ACCTGGACAC TAGGGTCAGG     1308
158 CGGGGTGCTG TGGTGGGGAG AGGCATGGCT GGGGTGGGGG TGGGGAGACC TGGTTGGCCG     1368
160 TGGTCCAGCT CTTGCCCCCT GTGTGAGTTG AGTCTCCTCT CTGAGACTGC TAAGTAGGGG     1428
162 CAGTGATGGT TGCCAGGACG AATTGAGATA ATATCTGTGA GGTGCTGATG AGTGATTGAC     1488
164 ACACAGCACT CTCTAAATCT TCCTTGTGAG GATTATGGGT CCTGCAATTC TACAGTTTCT     1548
166 TACTGTTTTG TATCAAAATC ACTATCTTTC TGATAACAGA ATTGCCAAGG CAGCGGGATC     1608
168 TCGTATCTTT AAAAAGCAGT CCTCTTATTC CTAAGGTAAT CCTATTAAAA CACAGCTTTA     1668
170 CAACTCCAT ATTACAAAAA AAAAAAAAAA AAA
174 (2) INFORMATION FOR SEQ ID NO: 2:
176     (i) SEQUENCE CHARACTERISTICS:
177         (A) LENGTH: 256 amino acids
178         (B) TYPE: amino acid
179         (D) TOPOLOGY: linear
181     (ii) MOLECULE TYPE: protein
183     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
186 1      5      10      15
188 Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
189      20      25      30
191 Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
192      35      40      45
194 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
195      50      55      60
197 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
198      65      70      75      80
200 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
201      85      90      95
203 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
204      100     105     110
206 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
207      115     120     125
209 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
210      130     135     140
212 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
213 145      150     155     160
215 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
216      165     170     175
218 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser

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219		180		185		190
221	Leu Arg Ile	Trp Lys Asn Thr	Glu Lys Glu Asn Ala	Thr Val Ala His		
222		195	200	205		
224	Leu Val Gly	Ala Leu Arg Ser	Cys Gln Met Asn Leu	Val Ala Asp Leu		
225		210	215	220		
227	Val Gln Glu	Val Gln Gln Ala	Arg Asp Leu Gln	Asn Arg Ser Gly	Ala	
228	225		230	235	240	
230	Met Ser Pro	Met Ser Trp	Asn Ser Asp	Ala Ser Thr	Ser Glu Ala	Ser
231		245	250	255		

VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]